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SEQUENCE LISTING

<110> Mirus Corporation
Wong, So
Wakefield, Darren
Sokoloff, Alex
Monahan, Sean
Sebestyen, Magdolna
Wolff, Jon
Higgs, Lori

<120> A COMPOUND FOR TARGETING TO HEPATOCYTES IN VIVO

<130> Mirus.014.06

<160> 36

<170> PatentIn version 3.1

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<213> Bacteriophage T7

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20 25 30

Leu Asp Gly Ser Asn Arg Asp Phe Asn Ile Pro Phe Glu Tyr Leu Ala
35 40 45

Arg Lys Phe Val Val Val Thr Leu Ile Gly Val Asp Arg Lys Val Leu
50 55 60

Thr Ile Asn Thr Asp Tyr Arg Phe Ala Thr Arg Thr Thr Ile Ser Leu
65 70 75 80

Thr Lys Ala Trp Gly Pro Ala Asp Gly Tyr Thr Thr Ile Glu Leu Arg
85 90 95

Arg Val Thr Ser Thr Thr Asp Arg Leu Val Asp Phe Thr Asp Gly Ser
100 105 110

Ile Leu Arg Ala Tyr Asp Leu Asn Val Ala Gln Ile Gln Thr Met His
115 120 125

Val Ala Glu Glu Ala Arg Asp Leu Thr Thr Asp Thr Ile Gly Val Asn
130 135 140

Asn Asp Gly His Leu Asp Ala Arg Gly Arg Arg Ile Val Asn Leu Ala
145 150 155 160

Asn Ala Val Asp Asp Arg Asp Ala Val Pro Phe Gly Gln Leu Lys Thr
165 170 175

Met Asn Gln Asn Ser Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg
180 185 190

Asn Glu Ala Glu Thr Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu
195 200 205

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
210 215 220

Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr
225 230 235 240

Ala Thr Ser Ala Gly Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val
245 250 255

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Asn Ala Glu Asn Ser Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala
 260 265 270
 Glu Gln Gln Ala Asp Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn
 275 280 285
 Tyr Asn Gly Leu Ala Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val
 290 295 300
 Tyr Trp Lys Gly Asn Ile His Ala Asn Gly Arg Leu Tyr Met Thr Thr
 305 310 315 320
 Asn Gly Phe Asp Cys Gly Gln Tyr Gln Gln Phe Phe Gly Gly Val Thr
 325 330 335
 Asn Arg Tyr Ser Val Met Glu Trp Gly Asp Glu Asn Gly Trp Leu Met
 340 345 350
 Tyr Val Gln Arg Arg Glu Trp Thr Thr Ala Ile Gly Gly Asn Ile Gln
 355 360 365
 Leu Val Val Asn Gly Gln Ile Ile Thr Gln Gly Gly Ala Met Thr Gly
 370 375 380
 Gln Leu Lys Leu Gln Asn Gly His Val Leu Gln Leu Glu Ser Ala Ser
 385 390 395 400
 Asp Lys Ala His Tyr Ile Leu Ser Lys Asp Gly Asn Arg Asn Asn Trp
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 Tyr Ile Gly Arg Gly Ser Asp Asn Asn Asn Asp Cys Thr Phe His Ser
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 Tyr Val His Gly Thr Thr Leu Thr Leu Lys Gln Asp Tyr Ala Val Val
 435 440 445
 Asn Lys His Phe His Val Gly Gln Ala Val Val Ala Thr Asp Gly Asn
 450 455 460
 Ile Gln Gly Thr Lys Trp Gly Gly Lys Trp Leu Asp Ala Tyr Leu Arg
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 Asp Ser Phe Val Ala Lys Ser Lys Ala Trp Thr Gln Val Trp Ser Gly
 485 490 495
 Ser Ala Gly Gly Gly Val Ser Val Thr Val Ser Gln Asp Leu Arg Phe
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Arg Asn Ile Trp Ile Lys Cys Ala Asn Asn Ser Trp Asn Phe Phe Arg
515 520 525

Thr Gly Pro Asp Gly Ile Tyr Phe Ile Ala Ser Asp Gly Gly Trp Leu
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Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg Asn Glu Ala Glu Thr
35 40 45

Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu Ser Ser Thr Asn Ala
50 55 60

Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp Glu
65 70 75 80

Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr Ala Thr Ser Ala Gly
85 90 95

Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val Asn Ala Glu Asn Ser
100 105 110

Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala Glu Gln Gln Ala Asp
115 120 125

Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn Tyr Asn Gly Leu Ala
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 20 25 30

Leu Asp Gly Ser Asn Arg Asp Phe Asn Ile Pro Phe Glu Tyr Leu Ala
 35 40 45

Arg Lys Phe Val Val Val Thr Leu Ile Gly Val Asp Arg Lys Val Leu
 50 55 60

Thr Ile Asn Thr Asp Tyr Arg Phe Ala Thr Arg Thr Thr Ile Ser Leu
 65 70 75 80

Thr Lys Ala Trp Gly Pro Ala Asp Gly Tyr Thr Thr Ile Glu Leu Arg
 85 90 95

Arg Val Thr Ser Thr Thr Asp Arg Leu Val Asp Phe Thr Asp Gly Ser
 100 105 110

Ile Leu Arg Ala Tyr Asp Leu Asn Val Ala Gln Ile Gln Thr Met His
 115 120 125

Val Ala Glu Glu Ala Arg Asp Leu Thr Thr Asp Thr Ile Gly Val Asn
 130 135 140

Asn Asp Gly His Leu Asp Ala Arg Gly Arg Arg Ile Val Asn Leu Ala
 145 150 155 160

Asn Ala Val Asp Asp Arg Asp Ala Val Pro Phe Gly Gln Leu Lys Thr
 165 170 175

Met Asn Gln Asn Ser Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg
 180 185 190

Asn Glu Ala Glu Thr Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu
 195 200 205

Ser Ser Thr Asn Ala Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys
 210 215 220

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Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr
225 230 235 240

Ala Thr Ser Ala Gly Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val
245 250 255

Asn Ala Glu Asn Ser Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala
260 265 270

Glu Gln Gln Ala Asp Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn
275 280 285

Tyr Asn Gly Leu Ala Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val
290 295 300

Tyr Trp Lys Gly Asn
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20 25 30

Trp Gln Ala Arg Asn Glu Ala Leu Gln Phe Arg Asn Glu Ala Glu Thr
35 40 45

Phe Arg Asn Gln Ala Glu Gly Phe Lys Asn Glu Ser Ser Thr Asn Ala
50 55 60

Thr Asn Thr Lys Gln Trp Arg Asp Glu Thr Lys Gly Phe Arg Asp Glu
65 70 75 80

Ala Lys Arg Phe Lys Asn Thr Ala Gly Gln Tyr Ala Thr Ser Ala Gly
85 90 95

Asn Ser Ala Ser Ala Ala His Gln Ser Glu Val Asn Ala Glu Asn Ser
100 105 110

Ala Thr Ala Ser Ala Asn Ser Ala His Leu Ala Glu Gln Gln Ala Asp
115 120 125

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Arg Ala Glu Arg Glu Ala Asp Lys Leu Glu Asn Tyr Asn Gly Leu Ala
130 135 140

Gly Ala Ile Asp Lys Val Asp Gly Thr Asn Val Tyr Trp Lys Gly Asn
145 150 155 160

Ile His Ala Asn Gly Arg Leu Tyr Met Thr Thr Asn Gly Phe Asp Cys
165 170 175

Gly Gln Tyr Gln Gln Phe Phe Gly Gly Val Thr Asn Arg Tyr Ser Val
180 185 190

Met Glu Trp Gly Asp Glu Asn Gly Trp Leu Met Tyr Val Gln Arg Arg
195 200 205

Glu Trp Thr Thr Ala Ile Gly Gly Asn Ile Gln Leu Val Val Asn Gly
210 215 220

Gln Ile Ile Thr Gln Gly Gly Ala Met Thr Gly Gln Leu Lys Leu Gln
225 230 235 240

Asn Gly His Val Leu Gln Leu Glu Ser Ala Ser Asp Lys Ala His Tyr
245 250 255

Ile Leu Ser Lys Asp Gly Asn Arg Asn Asn Trp Tyr Ile Gly Arg Gly
260 265 270

Ser Asp Asn Asn Asn Asp Cys Thr Phe His Ser Tyr Val His Gly Thr
275 280 285

Thr Leu Thr Leu Lys Gln Asp Tyr Ala Val Val Asn Lys His Phe His
290 295 300

Val Gly Gln Ala Val Val Ala Thr Asp Gly Asn Ile Gln Gly Thr Lys
305 310 315 320

Trp Gly Gly Lys Trp Leu Asp Ala Tyr Leu Arg Asp Ser Phe Val Ala
325 330 335

Lys Ser Lys Ala Trp Thr Gln Val Trp Ser Gly Ser Ala Gly Gly Gly
340 345 350

Val Ser Val Thr Val Ser Gln Asp Leu Arg Phe Arg Asn Ile Trp Ile
355 360 365

Lys Cys Ala Asn Asn Ser Trp Asn Phe Phe Arg Thr Gly Pro Asp Gly
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Ile Tyr Phe Ile Ala Ser Asp Gly Gly Trp Leu Arg Phe Gln Ile His
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Glu	Thr	Lys	Gly	Phe	Arg	Asp	Glu	Ala	Lys	Arg	Phe	Lys	Asn	Thr	Ala
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Gly	Gln	Tyr	Ala	Thr	Ser	Ala	Gly
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Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
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Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
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Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala Gly
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<400> 26

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<400> 27

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<213> Bacteriophage T7

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Gly Phe Arg Asp Glu Ala Lys Arg Phe
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Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe
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Gly

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Glu Thr Lys Gly Phe Arg Asp Glu Ala Lys Arg Phe Lys Asn Thr Ala
 20 25 30

Gly